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(i) APPLICANT: NOBUTO YAMAMOTO

(ii) TITLE OF INVENTION: PREPARATION OF POTENT  
MACROPHAGE ACTIVATING FACTORS  
DERIVED FROM CLONED VITAMIN D  
BINDING PROTEIN AND ITS DOMAIN  
AND THEIR THERAPEUTIC USAGE  
FOR CANCER, HIV-INFECTION AND  
OSTEOPETROSIS

(iii) NUMBER OF SEQUENCES: 3

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: CAESAR, RIVISE, BERNSTEIN,  
COHEN & POKOTILOW, LTD.

(B) STREET: 1635 Market Street, 12th Floor

(C) CITY: Philadelphia

(D) STATE: PA

(E) COUNTRY: USA

(F) ZIP: 19103-2212

(v) **COMPUTER READABLE FORM:**

(A) MEDIUM TYPE: Diskette-3.5 inch, 1.44 Mb

(B) COMPUTER: IBM PC Compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: WORDPERFECT VERSION 4.2

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE: March 19, 1996

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/478,121

(B) FILING DATE: 07-JUNE-1995

**(viii) ATTORNEY/AGENT INFORMATION:**

(A) NAME: Robert S. Silver

(B) REGISTRATION NO.: 35,681

(C) REFERENCE/DOCKET NUMBER:Y1004/20002

**(ix) TELECOMMUNICATION INFORMATION:**

(A) TELEPHONE: (215) 567-2010

(B) TELEFAX: (215) 751-1142

(2) INFORMATION FOR SEQ ID NO: 1:

**[i] SEQUENCE CHARACTERISTICS:**

[A] LENGTH: 458 amino acids

[B] TYPE: amino acid

[D] TOPOLOGY: linear

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[ii] MOLECULE TYPE: protein
[ii] HYPOTHETICAL: no
[vi] ORIGINAL SOURCES:
[A] ORGANISM: Human
[B] INDIVIDUAL/ISOLATE: Vitamin D-binding protein
    (Gc protein)
[x] PUBLICATION INFORMATION:
[A] AUTHORS: Cooke, Nancy E., David, E Vivek
[B] TITLE: Serum Vitamin D-binding Protein is a
    Third Member of the Albumin and Alpha
    Fetoprotein Gene Family
[C] JOURNAL: J. Clinical Investigation
[D] VOLUME: 76
[E] ISSUE: 12
[F] PAGES: 2420-2424
[G] DATE: December, 1985
[K] RELEVANT RESIDUES IN SEQ ID NO:1: FROM 1-485

```

Leu	Glu	Arg	Gly	Arg	Asp	Tyr	Glu	Lys	Asn	Lys	Val	Cys	Lys	Glu	Phe	
			5						10					15		
Ser	His	Leu	Gly	Lys	Glu	Asp	Phe	Thr	Ser	Leu	Ser	Leu	Val	Leu	Tyr	
			20					25					30			
Ser	Arg	Lys	Phe	Pro	Ser	Gly	Thr	Phe	Glu	Gln	Val	Ser	Gln	Leu	Val	
		35					40					45				
Lys	Glu	Val	Val	Ser	Leu	Thr	Glu	Ala	Cys	Cys	Ala	Glu	Gly	Ala	Asp	
	50					55					60					
Pro	Asp	Cys	Tyr	Asp	Thr	Arg	Thr	Ser	Ala	Leu	Ser	Ala	Lys	Ser	Cys	
65					70					75					80	
Glu	Ser	Asn	Ser	Pro	Phe	Pro	Val	His	Pro	Gly	Thr	Ala	Glu	Cys	Cys	
				85					90					95		
Thr	Lys	Glu	Gly	Leu	Glu	Arg	Lys	Leu	Cys	Met	Ala	Ala	Leu	Lys	His	
			100					105					110			
Gln	Pro	Gln	Glu	Phe	Pro	Thr	Tyr	Val	Glu	Pro	Thr	Asn	Asp	Glu	Ile	
		115					120					125				
Cys	Glu	Ala	Phe	Arg	Lys	Asp	Pro	Lys	GLu	Tyr	Ala	Asn	Gln	Phe	Met	
	130					135					140					
Trp	Glu	Tyr	Ser	Thr	Asn	Tyr	Glu	Gln	Ala	Pro	Leu	Ser	Leu	Leu	Val	
145					150					155					160	
Ser	Tyr	Thr	Lys	Ser	Tyr	Leu	Ser	Met	Val	Gly	Ser	Cys	Cys	Thr	Ser	
				165					170					175		
Ala	Ser	Pro	Thr	Val	Cys	Phe	Leu	Lys	Glu	Arg	Leu	Gln	Leu	Lys	His	
			180					185					190			

Leu	Ser	Leu	Leu	Thr	Thr	Leu	Ser	Asn	Arg	Val	Cys	Ser	Gln	Tyr	Ala
		195					200					205			
Ala	Tyr	Gly	Glu	Lys	Lys	Ser	Arg	Leu	Ser	Asn	Leu	Ile	Lys	Leu	Ala
	210					215					220				
Gln	Lys	Val	Pro	Thr	Ala	Asp	Leu	Glu	Asp	Val	Leu	Pro	Leu	Ala	Glu
225					230					235					240
Asp	Ile	Thr	Asn	Ile	Leu	Ser	Lys	Cys	Cys	Glu	Ser	Ala	Ser	Glu	Asp
				245					250					255	
Cys	Met	Ala	Lys	Glu	Leu	Pro	Glu	His	Thr	Val	Lys	Leu	Cys	Asp	Asn
			260					265					270		
Leu	Ser	Thr	Lys	Asn	Ser	Lys	Phe	Glu	Asp	Cys	Cys	Gln	Glu	Lys	Thr
		275					280					285			
Ala	Met	Asp	Val	Phe	Val	Cys	Thr	Tyr	Phe	Met	Pro	Ala	Ala	Gln	Leu
	290					295					300				
Pro	Glu	Leu	Pro	Asp	Val	Arg	Leu	Pro	Thr	Asn	Lys	Asp	Val	Cys	Asp
305					310					315					320
Pro	Gly	Asn	Thr	Lys	Val	Met	Asp	Lys	Tyr	Thr	Phe	Glu	Leu	Ser	Arg
				325					330					335	
Arg	Thr	His	Leu	Pro	Glu	Val	Phe	Leu	Ser	Lys	Val	Leu	Glu	Pro	Thr
			340					345					350		
Leu	Lys	Ser	Leu	Gly	Glu	Cys	Cys	Asp	Val	Glu	Asp	Ser	Thr	Thr	Cys
		355					360					365			
Phe	Asn	Ala	Lys	Gly	Pro	Leu	Leu	Lys	Lys	Glu	Leu	Ser	Ser	Phe	Ile
	370					375					380				
Asp	Lys	Gly	Gln	Glu	Leu	Cys	Ala	Asp	Tyr	Ser	Glu	Asn	Thr	Phe	Thr
385					390					395					400
Glu	Tyr	Lys	Lys	Lys	Leu	Ala	Glu	Arg	Leu	Lys	Ala	Lys	Leu	Pro	Glu
				405					410					415	
Ala	Thr	Pro	Thr	Glu	Leu	Ala	Lys	Leu	Val	Asn	Lys	Arg	Ser	Asp	Phe
			420					425					430		
Ala	Ser	Asn	Cys	Cys	Ser	Ile	Asn	Ser	Pro	Pro	Leu	Tyr	Cys	Asp	Ser
		435					440					445			
Glu	Ile	Asp	Ala	Glu	Leu	Lys	Asn	Ile	Leu						
	450					455			458						

```

[2] INFORMATION FOR SEQ ID NO: 2:
[i] SEQUENCE CHARACTERISTICS:
  [A] LENGTH: 89 amino acids
  [B] TYPE: amino acid
  [D] TOPOLOGY: linear
[ii] MOLECULE TYPE: protein
[ii] HYPOTHETICAL: no
[vi] ORIGINAL SOURCES:
  [A] ORGANISM: Human
  [B] INDIVIDUAL/ISOLATE: Vitamin D-binding protein (Gc protein)
[x] PUBLICATION INFORMATION:
  [A] AUTHORS: Cooke, Nancy E., David, E Vivek
  [B] TITLE: Serum Vitamin D-binding Protein is a Third Member
of the Albumin and Alpha Fetoprotein Gene Family
  [C] JOURNAL: J. Clinical Investigation
  [D] VOLUME: 76
  [E] ISSUE: 12
  [F] PAGES: 2420-2424
  [G] DATE: December, 1985
  [K] RELEVANT RESIDUES IN SEQ ID NO:2: FROM 1 TO 4 and 5 TO 89

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Leu	Glu	Arg	Gly	Pro	Leu	Leu	Lys	Lys	Glu	Leu	Ser	Ser	Phe	Ile	Asp
			5						10					15	
Lys	Gly	Gln	Glu	Leu	Cys	Ala	Asp	Tyr	Ser	Glu	Asn	Thr	Phe	Thr	Glu
			20					25					30		
Tyr	Lys	Lys	Lys	Leu	Ala	Glu	Arg	Leu	Lys	Ala	Lys	Leu	Pro	Glu	Ala
		35					40					45			
Thr	Pro	Thr	Glu	Leu	Ala	Lys	Leu	Val	Asn	Lys	Arg	Ser	Asp	Phe	Ala
	50					55					60				
Ser	Asn	Cys	Cys	Ser	Ile	Asn	Ser	Pro	Pro	Leu	Tyr	Cys	Asp	Ser	Glu
65					70					75					80
Ile	Asp	Ala	Glu	Leu	Lys	Asn	Ile	Leu							
				85				89							

[3] INFORMATION FOR SEQ ID NO: 3:

[i] SEQUENCE CHARACTERISTICS:

[A] LENGTH: 88 amino acids

[B] TYPE: amino acid

[D] TOPOLOGY: linear

[ii] MOLECULE TYPE: protein

[ii] HYPOTHETICAL: no

[vi] ORIGINAL SOURCES:

[A] ORGANISM: Human

[B] INDIVIDUAL/ISOLATE: Vitamin D-binding protein (Gc protein)

[x] PUBLICATION INFORMATION:

[A] AUTHORS: Cooke, Nancy E., David, E Vivek

[B] TITLE: Serum Vitamin D-binding Protein is a Third Member of the Albumin and Alpha Fetoprotein Gene Family

[C] JOURNAL: J. Clinical Investigation

[D] VOLUME: 76

[E] ISSUE: 12

[F] PAGES: 2420-2424

[G] DATE: December, 1985

[K] RELEVANT RESIDUES IN SEQ ID NO:3: FROM 10 TO 94

Ile Ile Pro Val Glu Glu Glu Asn Pro Pro Leu Leu Lys Lys Glu Leu  
5 10 15

Ser Ser Phe Ile Asp Lys Gly Gln Glu Leu Cys Ala Asp Tyr Ser Glu  
20 25 30

Asn Thr Phe Thr Glu Tyr Lys Lys Lys Leu Ala Glu Arg Leu Lys Ala  
35 40 45

Lys Leu Pro Glu Ala Thr Pro Thr Glu Leu Ala Lys Leu Val Asn Lys  
50 55 60

Arg Ser Asp Phe Ala Ser Asn Cys Cys Ser Ile Asn Ser Pro Pro Leu  
65 70 75 80

Tyr Cys Asp Ser Glu Ile Asp Ala Glu Leu Lys Asn Ile Leu  
85 90 94